

Delaval, Jan

46767

From: Roark, Jessica
Sent: Monday, July 16, 2001 7:25 AM
To: Delaval, Jan
Subject: 09/484577

Good Morning Jan,

Please search from 09/484577

SEQ ID NO:3.

Please include interference. *ex hly*

Results on paper.

Thanks!

Jessica H. Roark

CM1 9B03
Mailbox 9E12
Art Unit 1644
703 605-1209

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 16, 2001, 07:35:55 ; Search time 1069.87 Seconds
(without alignments)
7243.256 Million cell updates/sec

Title: US-09-484-577a-3
Perfect score: 501
Sequence: 1 actccacagccctcaccga.....cagaatgcgcgatgatcat 501

Scoring table: IDENTITY_XUC
Gapop 10.0 , Gapext 1.0

Seatched: 1344157 seqs, 7733874588 residues

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*

- 1: gb_ba1:*
- 2: gb_ba2:*
- 3: gb_ba3:*
- 4: gb_in1:*
- 5: gb_in2:*
- 6: gb_in3:*
- 7: gb_om:*
- 8: gb_ov:*
- 9: gb_pat1:*
- 10: gb_pat2:*
- 11: gb_ph:*
- 12: gb_p11:*
- 13: gb_p12:*
- 14: gb_p13:*
- 15: gb_p14:*
- 16: em_ba1:*
- 17: em_ba2:*
- 18: em_fun:*
- 19: em_htgo_hum:*
- 20: em_htgo_inv:*
- 21: em_htgo_rod:*
- 22: em_htg_hum1:*
- 23: em_htg_hum2:*
- 24: em_htg_hum3:*
- 25: em_htg_hum4:*
- 26: em_htg_hum5:*
- 27: em_htg_hum6:*
- 28: em_htg_hum7:*
- 29: em_htg_hum8:*
- 30: em_htg_inv1:*
- 31: em_htg_inv2:*
- 32: em_htg_other:*
- 33: em_htg_rod:*
- 34: em_hum1:*
- 35: em_hum2:*
- 36: em_hum3:*
- 37: em_hum4:*
- 38: em_hum5:*
- 39: em_hum6:*
- 40: em_hum7:*
- 41: em_in:*
- 42: em_om:*
- 43: em_or:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	92.4	18.4	3526	2 AF273216	AF273216 Rhizobium
2	89.8	17.7	28804	3 SSU51197	US1197 Sphingomonas
3	89.8	17.7	28804	9 AR068625	AR068625 Sequence
4	86.8	17.3	15552	1 AF004049	AF004049 Xylella f
5	86	17.2	1428	3 NME391263	NME391263 Neisseria
6	86	17.2	4254	1 AF121772	AF121772 Neisseria
7	86	17.2	7824	3 NME391260	AJ391260 Neisseria
8	86	17.2	11381	1 AF002524	AF002524 Neisseria

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OM nucleic - nucleic search, using sw model

Run on: July 16, 2001, 07:35:55 ; Search time 1171.33 Seconds

(without alignments)
4043.164 Million cell updates/sec

Title: US-09-484-577A-3

Perfect score: 501

Sequence: 1 actctcagcctctcacgca.....cagaatgcggcgatgcatcat 501

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Seatched: 10228115 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*
10: gb_est10:*
11: gb_est11:*
12: gb_est12:*
13: gb_est13:*
14: gb_est14:*
15: gb_est15:*
16: gb_est16:*
17: gb_est17:*
18: gb_est18:*
19: gb_est19:*
20: gb_est20:*
21: gb_est21:*
22: gb_est22:*
23: gb_est23:*
24: gb_est24:*
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26: gb_est26:*
27: gb_est27:*
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30: gb_est30:*
31: gb_est31:*
32: gb_est32:*
33: gb_est33:*
34: gb_est34:*
35: gb_est35:*
36: gb_est36:*
37: gb_est37:*
38: gb_est38:*
39: gb_est39:*
40: gb_est40:*
41: gb_est41:*
42: gb_est42:*
43: gb_est43:*

44: em_esthum10:*
45: em_esthum11:*
46: em_esthum12:*
47: em_esthum13:*
48: em_esthum14:*
49: em_esthum15:*
50: em_esthum16:*
51: em_esthum17:*
52: em_esthum18:*
53: em_esthum19:*
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55: em_esthum21:*
56: em_esthum22:*
57: em_esthum23:*
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61: em_esthum27:*
62: em_esthum28:*
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73: em_esthum39:*
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78: em_esthum44:*
79: em_esthum45:*
80: em_esthum46:*
81: em_esthum47:*
82: em_esthum48:*
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85: em_esthum51:*
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88: em_esthum54:*
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111: em_esthum77:*
112: em_esthum78:*
113: em_esthum79:*
114: em_esthum80:*
115: em_esthum81:*
116: em_esthum82:*

117: gb_est48:*
118: gb_est49:*
119: gb_est50:*
120: gb_est51:*
121: gb_est52:*
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7

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252: gb_est172:*
253: gb_est173:*
254: gb_est174:*
255: gb_est175:*
256: gb_est176:*
257: gb_est177:*
258: gb_est178:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Match	Length	DB	ID	Description
No.							
C 1	60.6	12.1	932	219	CNS0070E	AL066254 Drosophila	
C 2	55	11.0	925	219	CNS0091P	AL053013 Drosophila	
C 3	44.8	8.9	508	31	AF630811	AF630811 AV630811	
C 4	43.6	8.7	772	218	AF075872	AF075872 Drosophila	
C 5	42	8.4	939	219	CNS004AB	AL054280 Drosophila	
C 6	40.8	8.4	932	219	CNS0072Q	AL066742 Drosophila	
C 7	39.8	7.9	639	24	AI1770858	AI1770858 606059D06	
C 8	39.6	7.9	576	103	AI8819230	AI8819230 606075806	
C 9	39.6	7.9	645	219	CNS01213	AL101589 Drosophila	
C 10	39.6	7.9	692	219	CNS007WH	AL050923 Drosophila	
C 11	39.6	7.9	754	170	BF8969678	BF8969678 963014A09	
C 12	38.8	7.9	814	152	BG3102235	BG3102235 HVMSEC001	
C 13	38.8	7.7	604	166	BE253745	BE253745 HVMSEC000	
C 14	38.8	7.7	600	164	BE215392	BE215392 HY_CEB000	
C 15	38.6	7.7	844	219	CNS00052P	AL056652 Drosophila	
C 16	38.4	7.7	925	219	CNS00091P	AL053013 Drosophila	
C 17	38	7.6	265	151	ROL1662	ROL1662 yef76a03.s1	
C 18	38	7.6	765	187	BF616985	BF616985 HVMSEC001	
C 19	37.6	7.5	424	167	BE040013	BE040013 WHE0410.D	
C 20	37	7.4	392	32	AV644920	AV644920 AV644920	
C 21	37	7.4	393	32	AV644931	AV644931 AV644931	
C 22	37	7.4	434	136	BE497481	BE497481 WHE0753.A	
C 23	37	7.4	529	31	AV640485	AV640485 AV640485	
C 24	37	7.4	667	238	AZ11633	AZ11633 OSJNB011	
C 25	36.8	7.3	441	137	BE604637	BE604637 WHE1413-1	
C 26	36.8	7.3	510	137	BE858055	BE858055 5-7F-ZO P	
C 27	36.8	7.3	521	30	AV434008	AV434008 AV434008	
C 28	36.8	7.3	600	31	AV602736	AV602736 AV602736	
C 29	36.8	7.3	649	136	BE490046	BE490046 WHE0364.B	
C 30	36.8	7.3	1101	219	CNS017SY	AI108040 Drosophila	
C 31	36.6	7.3	542	152	BG322774	BG322774 EML14_A1	
C 32	36.6	7.3	543	168	BF705550	BF705550 RH12_4_E	
C 33	36.6	7.3	602	111	AW056288	AW056288 660006F10	
C 34	36.6	7.3	706	137	BE050138	BE050138 HVMSEC010	
C 35	36.6	7.3	734	115	AW348861	AW348861 GMS210010A	
C 36	36.6	7.3	930	144	BF065890	BF065890 HY_CEB001	
C 37	36.4	7.3	466	162	BE051079	BE051079 z7.1h09.b	
C 38	36.4	7.3	547	152	BG314210	BG314210 WHE2460_E	
C 39	36.4	7.3	750	218	AF075952	AF075952 AF075952	
C 40	36.4	7.2	1009	219	CNS010EW	AI090882 Drosophila	
C 41	36.2	7.2	291	167	BE404053	BE404053 WHE0403.A	
C 42	36.2	7.2	604	167	BE441916	BE441916 925009E04	
C 43	36.2	7.2	679	156	AW448165	AW448165 BRY_1330	
C 44	36.2	7.2	866	112	BG320801	BG320801 Zm04_01e1	
C 45	36.2	7.2	1101	219	CNS001QC	AL068542 Drosophila	

ALIGNMENTS

JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)

COMMENT Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see [http://www.fruitfly.org/The BDGP Drosophila melanogaster BAC library](http://www.fruitfly.org/The%20BDGP/drosophila_melanogaster_BAC_library.html) was prepared by Kazutoyo Osoegawa and Aaron Mammosser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPci1-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES
source Location/Qualifiers
1..932
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RPci1-98"
/clone="BAC14ID21"
/note="end : TET3"

BASE COUNT 421 a 135 c 96 g 50 t 230 others

ORIGIN

Query Match 12.1%; Score 60.6; DB 219; Length 932;
Best Local Similarity 29.7%; Pred.No. 5e-06;
Matches 77; Conservative 83; Mismatches 99; Indels 0; Gaps 0;

Dy 47 gcgcgagggggaaccgccgagcagtgccttcctcgccggccgcctcgaaattgtc 106
|:::|||||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 890 GATSTYGGGSSCYGCKCKGBSSHYGKCBGYYSBBKCBGGBKCKCGGBGSS 831
|:::|||||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 107 gagagccgcacatcccacccaggatacaaggccgcttgcttgcgcctgtttcac 166
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::
Db 830 GCKSBGCCSCGBCHGCVSCBSSGGGTSTCTTKKGYSBCKCKGYKCKTYKKRGK 771
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::
Qy 167 tgcgcgctgctgtggcgaggtctgcgcagatcgatcatcgttgtcttcgatccaaga 226
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::
Db 770 GGTCGSGKSGKSOTTBGCCTGCKMYBTATTGKTBTGTYRKYSGCSCSYGKBXCTYGCBS 711
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::
Qy 227 atcgtgcgcggagaccgtgttaaacttggttaacgcgcctcgaggtctggcgtagtgcgc 286
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::
Db 710 YGYSCKTCCGCKCGSKCTCKCTCBGCSISTGCTCSIKNSGTCYTGTGCTYSTYTC 651
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::
Yy 287 actaatgtccgagatygcc 305
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 16, 2001, 07:36:00 ; Search time 126.18 Seconds
(without alignments)
2493.095 Million cell updates/sec

Title: US-09-484-577a-3
Perfect score: 501
Sequence: 1 actctccagccctcaccga.....cagatgcggcagatcatcat 501

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Seatched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_0601:*

1: /SIDSI/gcgdata/geneseq/NA1980.DAT:*
2: /SIDSI/gcgdata/geneseq/NA1981.DAT:*
3: /SIDSI/gcgdata/geneseq/NA1982.DAT:*
4: /SIDSI/gcgdata/geneseq/NA1983.DAT:*
5: /SIDSI/gcgdata/geneseq/NA1984.DAT:*
6: /SIDSI/gcgdata/geneseq/NA1985.DAT:*
7: /SIDSI/gcgdata/geneseq/NA1986.DAT:*
8: /SIDSI/gcgdata/geneseq/NA1987.DAT:*
9: /SIDSI/gcgdata/geneseq/NA1988.DAT:*
10: /SIDSI/gcgdata/geneseq/NA1989.DAT:*
11: /SIDSI/gcgdata/geneseq/NA1990.DAT:*
12: /SIDSI/gcgdata/geneseq/NA1991.DAT:*
13: /SIDSI/gcgdata/geneseq/NA1992.DAT:*
14: /SIDSI/gcgdata/geneseq/NA1993.DAT:*
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21: /SIDSI/gcgdata/geneseq/NA2000.DAT:*
22: /SIDSI/gcgdata/geneseq/NA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	88.8	17.7	28804	17	AAT37329
C 2	88.8	17.7	28804	18	AAT92474
C 3	88.8	17.7	28804	20	AAV99812
C 4	88.8	17.7	28804	20	AAV81474
C 5	86	17.2	1305	21	AAZ54336
C 6	86	17.2	1428	21	AAZ54335
C 7	86	17.2	24158	21	AAAB1532
C 8	86	17.2	34980	21	AAAF21611
C 9	86	17.2	34980	21	AAAF21612
C 10	86	17.2	837096	21	AAAB1489
C 11	51.6	10.3	5120	18	AAAT73218

12	51.6	10.3	5120	21	AAZ88585
13	47.8	9.5	6400	20	AAZ22701
14	45	9.0	7184	15	AAO70050
15	43.4	8.7	7183	11	AAO06074
16	43	8.6	24379	18	AAQ93095
17	43	8.6	24379	19	AAV25925
18	39	7.8	1998	22	AAAF72013
19	37.6	7.5	10732	21	AAAI0594
20	37.2	7.4	1194	17	AAAT5855
21	37.2	7.4	4496	17	AAV58553
22	37.2	7.4	58857	21	AAV58471
23	37	7.4	1951	19	AAV11459
24	37	7.4	1981	21	AAZ50482
25	36.2	7.2	16020	21	AAV39283
26	36	7.2	1136	21	AAAC47742
27	35.8	7.1	836	19	AAV62157
28	35.8	7.1	3765	21	AAV5782
29	35.8	7.1	53500	21	AAV5842
30	35.8	7.1	117213	19	AAV62176
31	35.4	7.1	48300	22	AAAF61281
32	35	7.0	2025	21	AAV49036
33	34.8	6.9	1470	21	AAV38391
34	34.8	6.9	11279	21	AAV38391
35	34.6	6.9	8438	15	AAV38389
36	34.4	6.9	1830	22	AAV38389
37	34.4	6.9	10095	19	AAV38389
38	34.2	6.8	10095	19	AAV38389
39	34	6.8	1758	21	AAV38389
40	34	6.8	1758	21	AAV38389
41	34	6.8	2061	10	AAV38389
42	34	6.8	3632	17	AAV38389
43	34	6.8	3632	19	AAV38389
44	34	6.8	49272	20	AAV38389
45	34	6.8	114955	20	AAV38389

ALIGNMENTS

RESULT 1	AAAT37329/c	standard; DNA: 28804 BP.
ID	AAAT37329;	
XX		
AC	AAAT37329;	
XX		
DT	30-NOV-1996	(first entry)
XX		
DE	Sphingian biosynthetic gene region.	
XX		
KW	Sphingian; polysaccharide; spsB gene; glucosyl-IP-transferase; ds.	
XX		
OS	Sphingomonas strain S88 (ATCC 31554).	
XX		
FH	Location/Qualifiers	
FT	complement (1942..1944)	
FT	/tag= a	
FT	/codon_start= 1942..1944	
FT	/note= "spsB gene putative initiation codon"	
FT	complement (3311..3313)	
FT	/tag= b	
FT	/codon_start= 3311..3313	
FT	/note= "spsB gene putative initiation codon"	
FT	complement (5323..5325)	
FT	/tag= c	
FT	/codon_start= 5323..5325	
FT	/note= "spsB gene putative initiation codon"	
FT	5526..5528	
FT	/tag= d	
FT	/codon_start= 5526..5528	
FT	/note= "spsO gene putative initiation codon"	
FT	complement (7076..7078)	
FT	/tag= e	
FT	/codon_start= 7076..7078	

A. pleuropneumonia
Pseudomonas fluores
pix gene of Pasteu
Sequence encoding
Streptomyces fireo
Streptomyces roseo
Corynebacterium q1
Gene encoding a su
Streptomyces prist
Streptomyces prist
Nucleotide sequenc
C. acidivorans gam
Corn sulphate perm
Streptomyces nogal
Zea mays DNA fragm
HSV-2 strain SB5 C
Nucleotide sequenc
Complete nucleotid
HSV-2 strain SB5 C
N. magdall bacter
DNA encoding a hig
Pseudomonas sp. WF
Pseudomonas sp. WF
DNA encoding pseud
Wheat Nph2-2 prote
Mycobacterium tube
CDNA clone p17 enc
Rat hepatocyte nuc
Sequence encoding
T. thermophilus ga
Thermus thermophil
Mycobacteriophage
Human adenosine A1

FT	/note="spst gene putative initiation codon"	7588..7590
FT	/tag= f	
FT	/codon_start= 7588..7590	
FT	/note="spsk gene putative initiation codon"	
FT	/tag= g	8643..8645
FT	/codon_start= 8643..8645	
FT	/note="spst gene putative initiation codon"	
FT	complement (10938..10940)	
FT	/tag= h	
FT	/codon_start= 10938..10940	
FT	/note="spsd gene putative initiation codon"	
FT	/tag= i	11569..11571
FT	/codon_start= 11569..11571	
FT	/note="spsf gene putative initiation codon"	
FT	/tag= j	12886..12888
FT	/codon_start= 12886..12888	
FT	/note="spsd gene putative initiation codon"	
FT	/tag= k	15165..15167
FT	/codon_start= 15165..15167	
FT	/note="spse gene putative initiation codon"	
FT	/tag= l	15883..15885
FT	/codon_start= 15883..15885	
FT	/note="urf12 gene putative initiation codon"	
FT	/tag= m	16748..16750
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FT	/note="urf26 gene putative initiation codon"	
FT	complement (21082..21084)	
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FT	/codon_start= 21082..21084	
FT	/note="sarb gene putative initiation codon"	
FT	/tag= o	23338..23340
FT	/product= glucosyl IP-transferase	
FT	/tag= p	
FT	/codon_start= 23338..23340	
FT	/note="rnsa gene putative initiation codon"	
FT	/tag= q	24113..24115
FT	/codon_start= 24113..24115	
FT	/note="rnsC gene putative initiation codon"	
FT	/tag= r	24683..24685
FT	/codon_start= 24683..24685	
FT	/note="rnsB gene putative initiation codon"	
FT	/tag= s	25744..25746
FT	/codon_start= 25744..25746	
FT	/note="rnsD gene putative complement (27534..27536)	
FT	/tag= t	
FT	/codon_start= 27534..27536	
FT	/note="urf11 gene putative initiation codon"	
FT	/tag= u	27747
FT	/codon_start= 27747..27749	
FT	/note="urf14 gene putative initiation codon"	
PN	EF728841-A2.	
PN	28-AUG-1996.	
PD	24-JAN-1996;	96EP-0300467.
PF	24-JAN-1995;	95US-0377440

XX (SHIN-) SHINETSU BIO INC.
PA (SHIE) SHINETSU CHEM CO LTD.
XX
PI Armentrout RW, Mikolajczak M, Pollock TJ, Thorne L,
PI Yamazaki M;
DR WPI: 1996-386292/39.
DR P-PSDB: AAM03997.
XX
PT New isolated DNA from *Sphingomonas* sp. - used for transforming
PT recipient bacteria to obtain hyper-producers of sphingian
PT polysaccharide(s).
XX
PS Claim 32; Page 56-70; 105pp; English.
XX
XX A 28.8 kb chromosomal fragment of *Sphingomonas* strain S88 was
XX isolated on the basis of its ability to restore sphingian
CC biosynthetic capability to *Sphingomonas* mutant S88m260. It
CC contains 23-25 genes, including sps genes coding for biosynthesis of
CC the polysaccharide sphingian, rbs genes coding for dTDP-(L)ribose
CC biosynthesis, atdB genes coding for a transport function and some
CC unidentified open translation reading frames (urf). The spsB gene
CC was identified that is believed to code for glucosyl IP-transferase
CC (AAM03997), an enzyme catalysing the first step of assembly of
CC sphingian carbohydrates. DNA fragments of S88 can be inserted into
CC a vector in multiple copies and used to produce engineered bacteria
XX that are hyper-producers of sphingian.
XX
50 Sequence 28804 BP; 4974 A; 9806 C; 9228 G; 4796 T; 0 other;

	Query Match	17.7%	Score 88.8;	Df 17;	Length 28804;	
	Best Local Similarity	56.5%;	Pred. No. 2,3e-13;			
	Matches 165;	Conservative	0;	Mismatches 127;	Indels	0; Gaps
OY	80	tccgcgacggcgccgcctcgaattgtcgagacgcgcgcatactccaacgcgcgaactcacg	139			
DB	18808	TTCCTGCGGGCGCGCCTCGAGATCATCAACGTCGGGTGTCCGCCACCAGCGGCCTCACCC	18749			
OY	140	gccgccttgcttgcctgcgccttgttcactatgcgcgcgcygagtggttgaggcggtctcgcaagatc	199			
DB	18748	GCCCGGGTATGTTGGCGGGGGTGCGGATCCACACCGCTGGCTGGCAATCGGCCCGTc	18689			
OY	200	gacatcatgtctcttcgatccaccagaagaatcgtgcgcggcgagacctgttaagtctgttcag	259			
DB	18688	GAACTGCTGGCCCCGACGACGAGGGCCGCATCGCCCATCGCGGAGACCAAGATCTGCAG.	18629			
OY	260	cgcctcgaagtcgcgcgttgctgcggcgcaactcatgtctcgcgtaggcacaacccgtcaagyc	319			
DB	18628	TCCCCCGAAGAAGGGATTCTCTCCGGCCATTCTGTGGCGAAGGGGAGGAAGATTCAAG	18569			
OY	320	ggcgcagatctatcgaatcgatgatccatccgcgcgtygtctgatatgttcgc	371			
DB	18568	GCGCAGCTCTGATCAGCTTCATCCACCATTGTCGGCAGACCGCAACCCGCCG	18517			
RESULT	2					
	AAT92474/C					
ID	AAT92474	standard; DNA; 28804 BP.				
XX	AAT92474;					
XX	04-FEB-1998	(first entry)				
DE	Sphingomonas genus microbe isolated DNA sequence producing sphingan.					
XX	Sphingomonas microbe; sphingan polysaccharide biosynthesis gene;					
KW	sphingan S-88; spsB gene; ss.					
OS	Sphingomonas sp.					
PN	JP09252775-A.					

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 16, 2001, 07:36:00 : Search time 62.76 seconds
(without alignments)
1478.895 Million cell updates/sec

Title: US-09-484-577a-3

Perfect score: 501
Sequence: 1 actctcagcgtctcaccga.....cagaatcgcgatgatcat 501

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Sequences: 317530 seqs, 92630169 residues

Total number of hits satisfying chosen parameters: 635060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: Issued_Patents_NA.*
2: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*
3: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
5: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
6: /cgn2_6/ptodata/2/ina/Backfillseq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query Match	Length	ID	Description
1	88.8	17.7	28804	2	US-08-592-874-1
2	88.8	17.7	28804	3	US-09-096-942-2
3	88.8	17.7	28804	3	US-09-096-867-2
4	51.6	10.3	5120	2	US-08-772-270A-6
5	51.6	10.3	8370	2	US-08-488-706-1
6	37	7.4	1951	3	US-08-922-865-1
7	34.6	6.9	8438	1	US-07-945-283-1
8	34.4	6.9	1879	2	US-08-403-852D-5
9	34.4	6.9	1879	3	US-08-510-646B-5
10	34.4	6.9	1879	4	US-09-231-818-5
11	34.2	6.8	10095	3	US-08-822-586-45
12	34.2	6.8	10095	3	US-08-078-222B-1
13	34	6.8	1758	2	US-08-661-330A-1
14	34	6.8	1758	2	US-08-661-330A-1
15	34	6.8	1758	2	US-08-661-330A-1
16	33.2	6.6	2293	1	US-08-614-217A-1
17	33.2	6.6	3004	1	US-08-604-913B-12
18	33.2	6.6	5970	4	US-09-320-878-21
19	33.2	6.6	5247	1	US-08-920-812-15
20	32.8	6.5	5247	1	US-08-920-827-15
21	32.8	6.5	5247	1	US-08-921-177-15
22	32.8	6.5	5247	1	US-08-362-577C-15
23	32.8	6.5	5247	2	US-08-920-828-15
24	32.4	6.5	3877	2	US-08-599-895-1
25	32.4	6.5	3877	2	US-09-211-290-1
26	32.4	6.5	3877	4	US-09-322-676-1
27	32.2	6.4	720	4	US-08-998-416-662

28	32.2	6.4	783	1	US-08-264-861A-11	Sequence 11, Appl
29	32.2	6.4	783	5	PCT-US95-07784-11	Sequence 11, Appl
30	32.2	6.4	1150	1	US-08-264-861A-10	Sequence 10, Appl
31	32.2	6.4	1150	5	PCT-US95-07784-10	Sequence 10, Appl
32	32	6.4	1365	4	US-09-310-892-1	Sequence 1, Appl
33	31.8	6.3	3292	4	US-09-320-878-22	Sequence 22, Appl
34	31.8	6.3	4465	2	US-08-620-605D-1	Sequence 1, Appl
35	31.8	6.3	4547	2	US-09-005-232A-1	Sequence 1, Appl
36	31.8	6.3	11907	4	US-08-061-376-4	Sequence 4, Appl
37	31.8	6.3	20235	1	US-07-642-0734C-3	Sequence 3, Appl
38	31.8	6.3	20235	3	US-08-439-009A-3	Sequence 3, Appl
39	31.8	6.3	38506	4	US-09-320-878-19	Sequence 19, Appl
40	31.6	6.3	80161	4	US-09-036-987A-11	Sequence 1, Appl
41	31.4	6.3	1151	1	US-07-704-288C-2	Sequence 2, Appl
42	31.4	6.3	1151	1	US-08-093-372-1	Sequence 1, Appl
43	31.4	6.3	1151	1	US-08-379-259-2	Sequence 2, Appl
44	31.4	6.3	1668	4	US-09-385-028-20	Sequence 20, Appl
45	31.4	6.3	2936	2	US-08-714-677-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-08-592-874-1/c
Sequence 1, Application US/08592874
Patent No. 5854034
GENERAL INFORMATION:
APPLICANT: POLLOCK, THOMAS J.
APPLICANT: YAMAZAKI, MOTOHIDE
APPLICANT: THORNE, LINDA
APPLICANT: MIKOLAJCZAK, MARCIA
APPLICANT: ARMENTROUT, RICHARD W.
TITLE OF INVENTION: DNA SEGMENTS AND METHODS FOR INCREASING
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESSES:
ADDRESSER: JULES E. GOLDBERG
STREET: 261 MADISON AVENUE
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10016-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,874
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/377,440
FILING DATE: 24-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: GOLDBERG, JULES E.
REGISTRATION NUMBER: 24,408
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-986-4090
TELEFAX: 212-818-9479
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 28804 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FRAGMENT TYPE: N-terminal
US-08-592-874-1

Query Match 17.7%; Score 88.8; DB 2; Length 28804;

